OIPE

RAW SEQUENCE LISTING   DATE: 06/01/2001
PATENT APPLICATION: US/09/645,415   TIME: 12:53:43

Input Set : A:\8002059a.app
Output Set: C:\CRF3\06012001\I645415.raw

Does Not Comply
Corrected Diskette Needed

```
 4 <110> APPLICANT: Bermudes, G.
 5        King, I.
 6        Clairmont, C.
 7        Lin, S.
 8        Belcourt, M.
10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
11        TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
14 <130> FILE REFERENCE: 8002-059
16 <140> CURRENT APPLICATION NUMBER: US/09/645,415    (C-->)
16 <141> CURRENT FILING DATE: 2000-08-24             (C-->)
16 <150> PRIOR APPLICATION NUMBER: 60/157,581
17 <151> PRIOR FILING DATE: 1999-10-04
19 <150> PRIOR APPLICATION NUMBER: 60/157,637
20 <151> PRIOR FILING DATE: 1999-10-04
22 <160> NUMBER OF SEQ ID NOS: 61
24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 26
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Forward primer
34 <400> SEQUENCE: 1
35  gaagatcttc cggaggaggg gaaatg                                26
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 44
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Reverse primer
45 <400> SEQUENCE: 2
46  cgggatccga gctcgagggc ccgggaaagg atctaagaag atcc            44
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 477
50 <212> TYPE: DNA
51 <213> ORGANISM: Homo sapiens
53 <220> FEATURE:
54 <221> NAME/KEY: CDS
55 <222> LOCATION: (1)...(474)
57 <400> SEQUENCE: 3
58  atg gta cgt agc tcc tct cgc act ccg tcc gat aag ccg gtt gct cat    48
59  Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
60   1               5                  10                  15
62  gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt    96
63  Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
64              20                  25                  30
66  cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag    144
```

```
 67  Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
 68           35                  40                  45
 70  ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg      192
 71  Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 72           50                  55                  60
 74  ttc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc      240
 75  Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
 76   65                  70                  75                  80
 78  atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc      288
 79  Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
 80                   85                  90                  95
 82  gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg      336
 83  Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 84                   100                 105                 110
 86  aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag      384
 87  Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 88           115                 120                 125
 90  aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat      432
 91  Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 92           130                 135                 140
 94  ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg              474
 95  Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 96  145                 150                 155
 98  taa                                                                  477
100  <210> SEQ ID NO: 4
101  <211> LENGTH: 158
102  <212> TYPE: PRT
103  <213> ORGANISM: Homo sapiens
105  <400> SEQUENCE: 4
106  Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
107   1                   5                  10                  15
108  Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
109                   20                  25                  30
110  Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
111           35                  40                  45
112  Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
113           50                  55                  60
114  Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
115   65                  70                  75                  80
116  Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
117                   85                  90                  95
118  Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
119                   100                 105                 110
120  Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
121           115                 120                 125
122  Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
123           130                 135                 140
124  Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
125  145                 150                 155
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Input Set : A:\8002059a.app
Output Set: C:\CRF3\06012001\I645415.raw

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127 <210> SEQ ID NO: 5
128 <211> LENGTH: 28
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Forward primer
135 <400> SEQUENCE: 5
136  ccgacgcgtt gacacctgaa aactggag                                   28
138 <210> SEQ ID NO: 6
139 <211> LENGTH: 29
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Reverse primer
146 <400> SEQUENCE: 6
147  ccgacgcgtg aaaggatctc aagaagatc                                  29
149 <210> SEQ ID NO: 7
150 <211> LENGTH: 543
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Fusion construct
157 <221> NAME/KEY: CDS
158 <222> LOCATION: (1)...(540)
160 <400> SEQUENCE: 7
161  atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct    48
162  Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
163  1               5                  10                  15
165  acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc    96
166  Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
167              20                  25                  30
169  gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag   144
170  Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
171          35                  40                  45
173  ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt   192
174  Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
175          50                  55                  60
177  gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg   240
178  Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
179  65                  70                  75                  80
181  atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat   288
182  Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
183              85                  90                  95
185  gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc   336
186  Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
187              100                 105                 110
189  aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act   384
190  Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
191              115                 120                 125
```

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Input Set : A:\8002059a.app
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```
193   ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt        432
194   Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
195        130                 135                 140
197   ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac        480
198   Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
199   145                 150                 155                 160
201   cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt        528
202   Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
203                     165                 170                 175
205   att atc gca ctg taa                                                    543
206   Ile Ile Ala Leu
207                     180
210   <210> SEQ ID NO: 8
211   <211> LENGTH: 180
212   <212> TYPE: PRT
213   <213> ORGANISM: Artificial Sequence
215   <220> FEATURE:
215   <223> OTHER INFORMATION:
215   <400> SEQUENCE: 8
216   Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
217   1               5                 10                  15
218   Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
219                   20                  25                  30
220   Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
221             35                  40                  45
222   Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
223             50                  55                  60
224   Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
225   65                  70                  75                  80
226   Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
227                   85                  90                  95
228   Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
229                   100                 105                 110
230   Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
231             115                 120                 125
232   Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
233             130                 135                 140
234   Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
235   145                 150                 155                 160
236   Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
237                   165                 170                 175
238   Ile Ile Ala Leu
239                     180
241   <210> SEQ ID NO: 9
242   <211> LENGTH: 801
243   <212> TYPE: DNA
244   <213> ORGANISM: Artificial Sequence
246   <220> FEATURE:
247   <223> OTHER INFORMATION: Fusion construct
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W--> 215
W--> 215

→ see item 11 on Erra Summary sheet

Please correct this error in subsequent sequences.

Please Not :
Use f n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequenc Listing to ensure that a corresponding explanati n is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Input Set : A:\8002059a.app
Output Set: C:\CRF3\06012001\I645415.raw

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249 <221> NAME/KEY: CDS
250 <222> LOCATION: (1)...(798)
252 <400> SEQUENCE: 9
253  atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct      48
254  Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
255   1               5                  10                  15
257  acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac      96
258  Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
259               20                  25                  30
261  aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt     144
262  Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
263               35                  40                  45
265  tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa     192
266  Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
267      50                  55                  60
269  gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc     240
270  Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
271   65                  70                  75                  80
273  tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct     288
274  Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
275                   85                  90                  95
277  ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act     336
278  Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
279               100                 105                 110
281  ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat     384
282  Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
283               115                 120                 125
285  gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt     432
286  Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
287               130                 135                 140
289  ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc     480
290  Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
291  145                 150                 155                 160
293  atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga     528
294  Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
295                   165                 170                 175
297  ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc     576
298  Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
299               180                 185                 190
301  caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg     624
302  Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
303               195                 200                 205
305  aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc     672
306  Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
307               210                 215                 220
309  tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga     720
310  Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
311  225                 230                 235                 240
313  att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa     768
```